

- cn+  
B<sub>1</sub>
- c) substituting said amino acid residue with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue, and which can be accommodated in the structure;
  - d) optionally repeating steps b) and c) recursively;
  - e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),
  - f) preparing the variant resulting from steps a) - e);
  - g) testing the pH dependent activity of said variant; and
  - h) optionally repeating steps a) - g) recursively; and
  - i) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

Please add the following new claims:

- B<sub>2</sub>
- 35. The method of claim 5, wherein said b) involves identifying an amino acid residue which is within 10 Å from an active site residue of the parent amylase in the three-dimensional structure of said parent, and which is involved in electrostatic or hydrophobic interactions with an active site residue.
  - 36. The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase at least 80% identical to SEQ ID NO:1.
  - 37. The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 90% identical to SEQ ID NO:1.
  - 38. The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 95% identical to SEQ ID NO:1.
  - 39. The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase is at least 98% identical to SEQ ID NO:1.
  - 40. The method of claim 5 or 35, wherein said parent maltogenic alpha-amylase has the amino acid sequence of SEQ ID NO:1.